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PCT09

RAW SEQUENCE LISTING   DATE: 06/12/2002
PATENT APPLICATION: US/09/744,100B   TIME: 14:37:31

Input Set : A:\BB1174 US PCT seqlist01.txt
Output Set: N:\CRF3\06122002\I744100B.raw

P-6

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 3 <110> APPLICANT: Cahoon, Rebecca
 4        Gutteridge, Steven
 5        Lee, Jian-Ming
 6        McGonigle, Brian
 7        Rafalski, Antoni
 9 <120> TITLE OF INVENTION: Ornithine Biosynthesis Enzymes
11 <130> FILE REFERENCE: BB-1174
13 <140> CURRENT APPLICATION NUMBER: 09/744,100B
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C--> `14 <141> CURRENT FILING DATE: 2002-04-04`
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16 <150> PRIOR APPLICATION NUMBER: PCT/US99/15931
17 <151> PRIOR FILING DATE: 1999-07-14
19 <150> PRIOR APPLICATION NUMBER: 60/093,209
20 <151> PRIOR FILING DATE: 1998-07-17
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ENTERED

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22 <160> NUMBER OF SEQ ID NOS: 12
24 <170> SOFTWARE: Microsoft Office 97
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 1201
28 <212> TYPE: DNA
29 <213> ORGANISM: Zea mays
31 <400> SEQUENCE: 1
32 tcgagctcga gctcgagccc cagtcaccgc agccatgctc ctcacgaaac cctacctctc   60
33 caactcgctc cttccagtcc catccccgcc gccgtcgggc cctactctca gctccaacca  120
34 tgcaagcccc cttgccgccc ctacttgccg tcgcagccgc ctccgcatct ccgccacatc  180
35 cacggctgcg ccgtctcctt cgtcggctgc cgctgccacc gcgtcgctga gtcgagtgga  240
36 cgtgctctcg gaggcgctcc cttttattca gcgattcaaa ggcaagacgg tggtggtcaa  300
37 gtacggcggt gcggcgatga agtccccgga gctgcaggcg tccgtgatcc gcgatctcgt  360
38 gctgctctcc tgcgtcggcc tccgccccgt gcttgttcac ggcggcggtc cggagattaa  420
39 ttcctggctg ctgcgcgtcg gcgtcgagcc gcagttccgc gacggcctcc gcgtcacgga  480
40 cgcgctcacc atggaggtcg tcgagatggt gctagtcggg aaggtcaaca aaaaccttgt  540
41 ttccctcatc aacatcgcgg gaggcaccgc cattggtctg tgcggcaagg acgcgcgcct  600
42 tatcaccgct cgcccgtctc caaatgcagc ggcgctggga ttcgtcggcg aggtttcgcg  660
43 cgtggacgcc accgtcctcc atcccatcat cgccgcgggc catatcccgg ttatcgccac  720
44 cgttgccgcc gacgagactg ggcaagccta taacatcaat gctgatacgg cggctggcga  780
45 gattgccgct gccgtgggcg ccgagaagct gctgttgctc acagatgtgt ctggcatttt  840
46 ggcggaccgt aatgaccctg ggagcctggt gaaggtggtc gacattgctg gggtgcggaa  900
47 gatggtggct gacgggaagg tagctggtgg gatgataccc aaggtggagt gttgtgttca  960
48 cgcccttgca caaggtgtac acaccgcaag tatcattgat gggcgtgttc cacactctct 1020
49 tctgcttgag attctcacag acgagggcac aggcaccatg atcactggct gagctgcttc 1080
50 atgccttcat ggtattttcc tgtgcctctt ttctcatatt gttgtgtttt atggctatgt 1140
51 agactaaact caagattgca ataagactac ctaagtttgg ttgaaaaaaa aaaaaaaaaa 1200
52 a                                                              1201
54 <210> SEQ ID NO: 2
55 <211> LENGTH: 345
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PATENT APPLICATION: US/09/744,100B   TIME: 14:37:31

Input Set : A:\BB1174 US PCT seqlist01.txt
Output Set: N:\CRF3\06122002\I744100B.raw

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56 <212> TYPE: PRT
57 <213> ORGANISM: Zea mays
59 <400> SEQUENCE: 2
60 Met Leu Leu Thr Lys Pro Tyr Leu Ser Asn Ser Leu Leu Pro Val Pro
61  1               5                   10                  15
63 Ser Pro Pro Pro Ser Gly Pro Thr Leu Ser Ser Asn His Ala Ser Pro
64           20                  25                  30
66 Leu Ala Ala Pro Thr Cys Arg Arg Ser Arg Leu Arg Ile Ser Ala Thr
67           35                  40                  45
69 Ser Thr Ala Ala Pro Ser Pro Ser Ser Ala Ala Ala Ala Thr Ala Ser
70       50                  55                  60
72 Leu Ser Arg Val Asp Val Leu Ser Glu Ala Leu Pro Phe Ile Gln Arg
73  65                  70                  75                  80
75 Phe Lys Gly Lys Thr Val Val Val Lys Tyr Gly Gly Ala Ala Met Lys
76               85                  90                  95
78 Ser Pro Glu Leu Gln Ala Ser Val Ile Arg Asp Leu Val Leu Leu Ser
79           100                 105                 110
81 Cys Val Gly Leu Arg Pro Val Leu Val His Gly Gly Gly Pro Glu Ile
82           115                 120                 125
84 Asn Ser Trp Leu Leu Arg Val Gly Val Glu Pro Gln Phe Arg Asp Gly
85       130                 135                 140
87 Leu Arg Val Thr Asp Ala Leu Thr Met Glu Val Val Glu Met Val Leu
88 145                 150                 155                 160
90 Val Gly Lys Val Asn Lys Asn Leu Val Ser Leu Ile Asn Ile Ala Gly
91               165                 170                 175
93 Gly Thr Ala Ile Gly Leu Cys Gly Lys Asp Ala Arg Leu Ile Thr Ala
94           180                 185                 190
96 Arg Pro Ser Pro Asn Ala Ala Ala Leu Gly Phe Val Gly Glu Val Ser
97           195                 200                 205
99 Arg Val Asp Ala Thr Val Leu His Pro Ile Ile Ala Ala Gly His Ile
100      210                 215                 220
102 Pro Val Ile Ala Thr Val Ala Ala Asp Glu Thr Gly Gln Ala Tyr Asn
103 225                 230                 235                 240
105 Ile Asn Ala Asp Thr Ala Ala Gly Glu Ile Ala Ala Ala Val Gly Ala
106           245                 250                 255
108 Glu Lys Leu Leu Leu Leu Thr Asp Val Ser Gly Ile Leu Ala Asp Arg
109           260                 265                 270
111 Asn Asp Pro Gly Ser Leu Val Lys Val Val Asp Ile Ala Gly Val Arg
112           275                 280                 285
114 Lys Met Val Ala Asp Gly Lys Val Ala Gly Gly Met Ile Pro Lys Val
115      290                 295                 300
117 Glu Cys Cys Val His Ala Leu Ala Gln Gly Val His Thr Ala Ser Ile
118 305                 310                 315                 320
120 Ile Asp Gly Arg Val Pro His Ser Leu Leu Leu Glu Ile Leu Thr Asp
121           325                 330                 335
123 Glu Gly Thr Gly Thr Met Ile Thr Gly
124           340                 345
126 <210> SEQ ID NO: 3
127 <211> LENGTH: 1186
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RAW SEQUENCE LISTING   DATE: 06/12/2002
PATENT APPLICATION: US/09/744,100B   TIME: 14:37:31

Input Set : A:\BB1174 US PCT seqlist01.txt
Output Set: N:\CRF3\06122002\I744100B.raw

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128 <212> TYPE: DNA
129 <213> ORGANISM: Oryza sativa
131 <220> FEATURE:
132 <221> NAME/KEY: unsure
133 <222> LOCATION: (613)
134 <223> OTHER INFORMATION: n = A, C, G, or T
136 <400> SEQUENCE: 3
137 gcacgagtac agcgccgccg ccgccgccat gctcctcgcg aagccccacc tctcctcctc   60
138 ctctttcctc ccatccacgc gggtgtctag ccccgctccg ggtcccaacc acgcaaagcc  120
139 catcgccgcc tctcccgccc ctcgacgctg cctccgtctc gccgtcacat ccgccgcggc  180
140 gccggctgct cgtcggcgg aggcggcggc ggcgctgagc cgcgtggatg tgctctcaga  240
141 ggcgctcccc ttcatccagc gcttcaaggg gaagaccgtg gtggtgaagt acggcggcgc  300
142 ggcgatgaag tcgccggagc tccaggcttc agtgatccgc gacctggtcc tcctctcgtg  360
143 cgtcggcctc caccccgtgc tcgtccacgg cggcgggccc gagatcaact cctggctgct  420
144 ccgcgtcggc gtcgagccgc agttccggaa cggcctccgc gtcactgacg cgctcaacat  480
145 ggaggtcgtc gagatggtgc tcgtccgcaa ggtcaacaaa gaactcctct ccctcatcaa  540
146 actcccgggg gggagcgccg taagtctctg ttggaaggaa gctcgcctcc tcaacgagcg  600
147 gccctccccg aangaaaagg gccttcggtt tgtcggcggg gtctggcgcg tggacgccac  660
148 cgtcctccac ccaatcatcg cctccggtca catcccggtc atcgccactg tgggcgccga  720
149 cgagaccggg caggcctaca acatcaacgc tgacacggcg gccggcgaga tcgccgccgc  780
150 ggtcggcgcg gagaagctgt tgctgctcac agatgtgtct ggaattctgg ccgaccgtaa  840
151 tgaccccggg agtctggtga aagagatcga cattgctggg gtgcggcaga tggtggccga  900
152 cgggcaggta gctggtggga tgataccgaa ggtggaatgc tgcgtgcgtg ccctcgcaca  960
153 gggcgtgcac actgcaagca tcatcgatgg gcgtgtcccg cactcgttgc tgctcgagat 1020
154 tctcacagat gagggcactg gcactatgat cactggctga ggtgattcat cccgtcgtgg 1080
155 tattctccgg tgcctctctt ctcatactgt aatgtaattt gcatttgata tgcctcatga 1140
156 ttgcaataag aattgtattc ctcaaaaaaa aaaaaaaaa aaaaaa         1186
158 <210> SEQ ID NO: 4
159 <211> LENGTH: 343
160 <212> TYPE: PRT
161 <213> ORGANISM: Oryza sativa
163 <220> FEATURE:
164 <221> NAME/KEY: UNSURE
165 <222> LOCATION: (195)
166 <223> OTHER INFORMATION: Xaa = ANY AMINO ACID
168 <400> SEQUENCE: 4
169 Met Leu Leu Ala Lys Pro His Leu Ser Ser Ser Ser Phe Leu Pro Ser
170  1               5                  10                  15
172 Thr Arg Val Ser Ser Pro Ala Pro Gly Pro Asn His Ala Lys Pro Ile
173                 20                  25                  30
175 Ala Ala Ser Pro Ala Pro Arg Arg Cys Leu Arg Leu Ala Val Thr Ser
176             35                  40                  45
178 Ala Ala Ala Pro Ala Ala Ser Ser Ala Glu Ala Ala Ala Ala Leu Ser
179         50                  55                  60
181 Arg Val Asp Val Leu Ser Glu Ala Leu Pro Phe Ile Gln Arg Phe Lys
182 65                  70                  75                  80
184 Gly Lys Thr Val Val Val Lys Tyr Gly Gly Ala Ala Met Lys Ser Pro
185                 85                  90                  95
187 Glu Leu Gln Ala Ser Val Ile Arg Asp Leu Val Leu Leu Ser Cys Val
```

```
188                     100                     105                     110
190 Gly Leu His Pro Val Leu Val His Gly Gly Gly Pro Glu Ile Asn Ser
191         115                     120                     125
193 Trp Leu Leu Arg Val Gly Val Glu Pro Gln Phe Arg Asn Gly Leu Arg
194     130                     135                     140
196 Val Thr Asp Ala Leu Asn Met Glu Val Val Glu Met Val Leu Val Arg
197 145                     150                     155                     160
199 Lys Val Asn Lys Glu Leu Leu Ser Leu Ile Lys Leu Pro Gly Gly Ser
200                     165                     170                     175
202 Ala Val Ser Leu Cys Trp Lys Glu Ala Arg Leu Leu Asn Glu Arg Pro
203         180                     185                     190
205 Ser Pro Xaa Glu Lys Gly Leu Arg Phe Val Gly Gly Val Trp Arg Val
206         195                     200                     205
208 Asp Ala Thr Val Leu His Pro Ile Ile Ala Ser Gly His Ile Pro Val
209     210                     215                     220
211 Ile Ala Thr Val Gly Ala Asp Glu Thr Gly Gln Ala Tyr Asn Ile Asn
212 225                     230                     235                     240
214 Ala Asp Thr Ala Ala Gly Glu Ile Ala Ala Ala Val Gly Ala Glu Lys
215                     245                     250                     255
217 Leu Leu Leu Leu Thr Asp Val Ser Gly Ile Leu Ala Asp Arg Asn Asp
218                     260                     265                     270
220 Pro Gly Ser Leu Val Lys Glu Ile Asp Ile Ala Gly Val Arg Gln Met
221         275                     280                     285
223 Val Ala Asp Gly Gln Val Ala Gly Gly Met Ile Pro Lys Val Glu Cys
224     290                     295                     300
226 Cys Val Arg Ala Leu Ala Gln Gly Val His Thr Ala Ser Ile Ile Asp
227 305                     310                     315                 320
229 Gly Arg Val Pro His Ser Leu Leu Leu Glu Ile Leu Thr Asp Glu Gly
230                     325                     330                     335
232 Thr Gly Thr Met Ile Thr Gly
233                     340
235 <210> SEQ ID NO: 5
236 <211> LENGTH: 1204
237 <212> TYPE: DNA
238 <213> ORGANISM: Glycine max
240 <400> SEQUENCE: 5
241  gcacgagatg atggcaggtg cagccaaaac cctaaccaat ctttgcccct ctttcccatt    60
242  cccaaccaaa ccccaaaacc aactcaccac tagccacgct ttcccttcca ctcgcctccg   120
243  ccaccgcgcc atttccgcgg tggcgaacgc ggcgcaacct ccactcgccg ccgccactgc   180
244  caccgagggt cagtaccgag tcgatgtgct ctcggagtcg ctccccttca tccagaaatt   240
245  ccgcggcaaa accatcgtcg tcaagtacgg cggcgccgcc atgaagtccc cggagctcca   300
246  ggcctccgtg atcaacgacc ttgtcctcct ctcctgcgtc ggcctccgcc ccgtcctggt   360
247  ccacggcggc ggccccgaga tcaactcctg gctcggccgc ctcaacatcc ccgccgtctt   420
248  ccgcgacggc ctccgcgtca ccgacgccga caccatggag atcgtctcca tggtcctcgt   480
249  cggaaaagtc aacaaaaccc tagtttctct aattaacaag gccggcgcca ccgccgtcgg   540
250  cctctctggc atggacggcc gcctcctcac cgcccgcccc gctcccaagg ccgccgacct   600
251  cggctacgtc ggcgaggtcg cacgcgtcga tcccgccgtc ctccgctccc taatcgacac   660
252  cagccacatc cccgtcgtca cctccgtcgc cgccgatgaa tccggacagc cctacaacat   720
253  caacgccgac accgtcgccg gagaattggc agcgtcgctc ggcgcggaga agctgattct   780
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254 gctgaccgat gtggcgggaa ttctggaaga tcggaacgac cctgacagct tggtgaagaa  840
255 gattgacata aaaggagtga agaaaatgat ggaagatgga aaagttggtg gtggaatgat  900
256 acctaaggtt aattgttgcg ttaggtcctt ggcgcaaggg gttattacag cgagtattat  960
257 tgatggtagg gttccgcatt ctttgttgct tgagattttg actgatgaag gtgctggaac 1020
258 tatgataact ggataagttt atttatttat ggtgtttgga ttttttcttt tcaatcaagc 1080
259 cttgagttga ggttgcattg cagcacttgt tttgttagag attggtgatt gtttttaagt 1140
260 gcgtgtaatg tgagagatgg ttgaattgaa ttgaatgttt cagaaaaaaa aaaaaaaaaa 1200
261 aaaa                                                              1204
263 <210> SEQ ID NO: 6
264 <211> LENGTH: 342
265 <212> TYPE: PRT
266 <213> ORGANISM: Glycine max
268 <400> SEQUENCE: 6
269 Met Met Ala Gly Ala Ala Lys Thr Leu Thr Asn Leu Cys Pro Ser Phe
270  1               5                  10                  15
272 Pro Phe Pro Thr Lys Pro Gln Asn Gln Leu Thr Thr Ser His Ala Phe
273             20                  25                  30
275 Pro Ser Thr Arg Leu Arg His Arg Ala Ile Ser Ala Val Ala Asn Ala
276         35                  40                  45
278 Ala Gln Pro Pro Leu Ala Ala Ala Thr Ala Thr Glu Gly Gln Tyr Arg
279     50                  55                  60
281 Val Asp Val Leu Ser Glu Ser Leu Pro Phe Ile Gln Lys Phe Arg Gly
282 65                  70                  75                  80
284 Lys Thr Ile Val Val Lys Tyr Gly Gly Ala Ala Met Lys Ser Pro Glu
285                 85                  90                  95
287 Leu Gln Ala Ser Val Ile Asn Asp Leu Val Leu Leu Ser Cys Val Gly
288             100                 105                 110
290 Leu Arg Pro Val Leu Val His Gly Gly Gly Pro Glu Ile Asn Ser Trp
291         115                 120                 125
293 Leu Gly Arg Leu Asn Ile Pro Ala Val Phe Arg Asp Gly Leu Arg Val
294     130                 135                 140
296 Thr Asp Ala Asp Thr Met Glu Ile Val Ser Met Val Leu Val Gly Lys
297 145                 150                 155                 160
299 Val Asn Lys Thr Leu Val Ser Leu Ile Asn Lys Ala Gly Ala Thr Ala
300                 165                 170                 175
302 Val Gly Leu Ser Gly Met Asp Gly Arg Leu Leu Thr Ala Arg Pro Ala
303             180                 185                 190
305 Pro Lys Ala Ala Asp Leu Gly Tyr Val Gly Glu Val Ala Arg Val Asp
306         195                 200                 205
308 Pro Ala Val Leu Arg Ser Leu Ile Asp Thr Ser His Ile Pro Val Val
309     210                 215                 220
311 Thr Ser Val Ala Ala Asp Glu Ser Gly Gln Pro Tyr Asn Ile Asn Ala
312 225                 230                 235                 240
314 Asp Thr Val Ala Gly Glu Leu Ala Ala Ser Leu Gly Ala Glu Lys Leu
315             245                 250                 255
317 Ile Leu Leu Thr Asp Val Ala Gly Ile Leu Glu Asp Arg Asn Asp Pro
318         260                 265                 270
320 Asp Ser Leu Val Lys Lys Ile Asp Ile Lys Gly Val Lys Lys Met Met
321             275                 280                 285
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 06/12/2002
PATENT APPLICATION: US/09/744,100B   TIME: 14:37:32

Input Set : A:\BB1174 US PCT seqlist01.txt
Output Set: N:\CRF3\06122002\I744100B.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 613
Seq#:4; Xaa Pos. 195
Seq#:7; N Pos. 492,493,494,495,496,497,498,499,500,501,502,503,504,505,506
Seq#:7; N Pos. 507,508,509,510,511,512,513,514,515,516,517,518,519,520,521
Seq#:7; N Pos. 522,523,524,525,526,527,528,529,530,531,532,533,534,535,536
Seq#:7; N Pos. 537,538,539,540,541,542
Seq#:8; Xaa Pos. 133,144,145,146,147,148,149,150,151,152,153,154,155,156
Seq#:8; Xaa Pos. 157,158,159,160
Seq#:12; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,24
Seq#:12; Xaa Pos. 25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43
Seq#:12; Xaa Pos. 44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,60,61,63,64
Seq#:12; Xaa Pos. 65,66,67,75,81,83,87,107,118,134,136,137,138,139,140,141
Seq#:12; Xaa Pos. 144,152,153,156,158,163,168,170,174,175,176,178,179,181
Seq#:12; Xaa Pos. 182,184,185,186,187,188,191,192,193,196,198,199,200,201
Seq#:12; Xaa Pos. 203,204,207,209,211,212,213,214,217,218,219,221,222,223
Seq#:12; Xaa Pos. 228,229,230,232,236,239,247,251,254,255,261,263,267,271
Seq#:12; Xaa Pos. 274,277,282,283,286,290,292,293,294,296,298,306,310,311
Seq#:12; Xaa Pos. 317,340